This listing of claims will replace all prior versions, and listings, of claims in the application:

## LISTING OF CLAIMS

1.  *(currently amended)*        A method of determining the copy number (CN) of a first nucleotide sequence I (NucSeqI) in a sample using an amplification technique, said method comprising the steps of:

(1)      adding to the sample nucleotides, primers, polymerase, probes and optionally, any additional reagents required for amplification;

(2)      performing one or more amplification cycles to amplify the NucSeqI, wherein the sample comprises a chromosome-derived second nucleotide sequence II (NucSeqII), and the following amplification steps are carried out:

(a)      NucSeqI is amplified,

(b)      NucSeqII is amplified,

(c)      a third nucleotide sequence I' (NucSeqI') corresponding to NucSeqI and present in a control sample is amplified at multiple dilutions, and

(d)      a fourth nucleotide sequence II' (NucSeqII') corresponding to NucSeqII and present in a control sample is amplified at multiple dilutions,

wherein

(i)      the ratio of concentration of NucSeqI' [[and]] to the concentration of NucSeqII' is known,

(ii)      standard curves $SC_I$ and $SC_{II}$ comprising at least two reference points are generated by wherein amplification of [[the]] NucSeqI' and NucSeqII' at multiple dilutions results in the generation of standard curves SCI and SCII, respectively, at multiple dilutions,

(iii)      at least one pair of amplification reactions (a) and (b) or (c) and (d) is performed in a single container and monitored by fluorescence during amplification, and

(iv)      NucSeqI' and NucSeqII' are localized on a single vector; and

(3)      determining from the results of the amplifications of step (2) such that the concentrations of NucSeqI and NucSeqII are determined by using the respective standard curves $SC_I$ and $SC_{II}$, to obtain the relative such that copy number CN of NucSeqI relative with respect to NucSeqII is determined using by the formula:

$$\text{relative CN} = \frac{\text{Conc-I}_{SCI}}{\text{Conc-II}_{SCII}}$$

wherein, in said formula,

(i)     "relative CN" is the ratio of the ~~relative copy number~~ CN of NucSeqI relative to the CN of NucSeqII~~)~~ in the sample;

(ii)     "Conc-I$_{SCI}$" is the concentration of NucSeqI determined ~~using~~ from standard curve SC$_I$; and

(iii)     "Conc-II$_{SCII}$" is the concentration of NucSeqII determined ~~using~~ from standard curve SC$_{II}$[[, and]]

~~wherein at least one pair of amplification reactions selected from (a) and (b), and (c) and (d) is performed in a single container and monitored spectrophotometrically during amplification, and NucSeqI' and NucSeqII' are localized on a single vector.~~

2. (***currently*** *amended*)      A method for determining the absolute CN of a nucleotide sequence NucSeqI in a sample, comprising:

(a)     determining the relative CN using the method of ~~according to~~ claim 1~~8~~, and ~~wherein an absolute copy number is determined by~~

(b)     multiplying the relative CN by the absolute CN ~~number of copies~~ of NucSeqII per cell.

3. *(previously presented)*      A method according to claim 1, wherein at least two different NucSeqI' sequences used for measuring a corresponding number of different NucSeqI sequences are localized on a single vector.

4. *(previously presented)*      A method according to claim 1 wherein the sequences of NucSeqI and NucSeqI' are the same.

5. *(previously presented)*      A method according to claim 1 wherein the sequences of NucSeqII and NucSeqII' are the same.

6. *(previously presented)*      A method according to claim 2, wherein at least two different NucSeqI' sequences used for measuring a corresponding number of different NucSeqI are localized on a single vector.

7. *(previously presented)*        A method according to claim 2 wherein the sequences of NucSeqI and the NucSeqI' are the same.

8. *(previously presented)*        A method according to claim 3 wherein the sequences of NucSeqI and the NucSeqI' are the same.

9. *(previously presented)*        A method according to claim 6 wherein the sequences of NucSeqI and the NucSeqI' are the same.

10. *(previously presented)*        A method according to claim 2 wherein the sequences of NucSeqII and the NucSeqII' are the same.

11. *(previously presented)*        A method according to claim 3 wherein the sequences of NucSeqII and the NucSeqII' are the same.

12. *(previously presented)*        A method according to claim 4 wherein the sequences of NucSeqII and the NucSeqII' are the same.

13. *(previously presented)*        A method according to claim 6 wherein the sequences of NucSeqII and the NucSeqII' are the same.

14. *(previously presented)*        A method according to claim 7 wherein the sequences of NucSeqII and the NucSeqII' are the same.

15. *(previously presented)*        A method according to claim 8 wherein the sequences of NucSeqII and the NucSeqII' are the same.

16. *(previously presented )*        A method according to claim 9 wherein the sequences of NucSeqII and the NucSeqII' are the same.

17. *(new)*        A method according to claim 1, wherein the sample is derived from cells.

18. *(new)*        A method according to claim 17, wherein an absolute CN of NucSeqII per cell is known.

19. *(new)*        A method according to claim 18, wherein at least two different NucSeqI' sequences used for measuring a corresponding number of different NucSeqI are localized on a single vector.

20. *(new)*      A method according to claim 18, wherein the sequences of NucSeqI and the NucSeqI' are the same.

21. *(new)*      A method according to claim 18 wherein the sequences of NucSeqII and the NucSeqII' are the same.

22. *(new)*      A method according to claim 19 wherein the sequences of NucSeqII and the NucSeqII' are the same.

23. *(new)*      A method according to claim 20 wherein the sequences of NucSeqII and the NucSeqII' are the same.

24. *(new)*      A method of determining the CN of a first nucleotide sequence I (NucSeqI) in a sample using an amplification technique, said method comprising the steps of:

(1)      adding to the sample nucleotides, primers, polymerase, probes and optionally, any additional reagents required for amplification;

(2)      performing one or more amplification cycles to amplify NucSeqI,

wherein the sample comprises a second nucleotide sequence II (NucSeqII), and the following amplification steps are carried out:

(a)      NucSeqI is amplified,

(b)      NucSeqII is amplified,

(c)      a third nucleotide sequence I' (NucSeqI') corresponding to NucSeqI and present in a control sample is amplified at multiple dilutions, and

(d)      a fourth nucleotide sequence II' (NucSeqII') corresponding to NucSeqII and present in a control sample is amplified at multiple dilutions,

wherein

(i)      the ratio of the concentration of NucSeqI' to the concentration of NucSeqII' is known,

(ii)      standard curves $SC_I$ and $SC_{II}$ comprising at least two reference points are generated by amplification of NucSeqI' and NucSeqII', respectively, at multiple dilutions,

(iii)      at least one pair of amplification reactions (a) and (b) or (c) and (d) is performed in a single container and monitored by fluorescence during amplification, and

(iv)    NucSeqI' and NucSeqII' are localized on a single vector; and

(3)    determining from the results of the amplifications of step (2) the concentrations of NucSeqI and NucSeqII  using the respective standard curves $SC_I$ and $SC_{II}$, to obtain the relative CN of NucSeqI with respect to NucSeqII, by the formula:

$$\text{relative CN} = \frac{\text{Conc-I}_{SCI}}{\text{Conc-II}_{SCII}}$$

wherein, in said formula,

(a)    "relative CN" is the CN of NucSeqI relative to the CN of NucSeqII in the sample;

(b)    "Conc-I$_{SCI}$" is the concentration of NucSeqI determined from standard curve $SC_I$; and

(c)    "Conc-II$_{SCII}$" is the concentration of NucSeqII determined from standard curve $SC_{II}$.

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